

Fig. 1

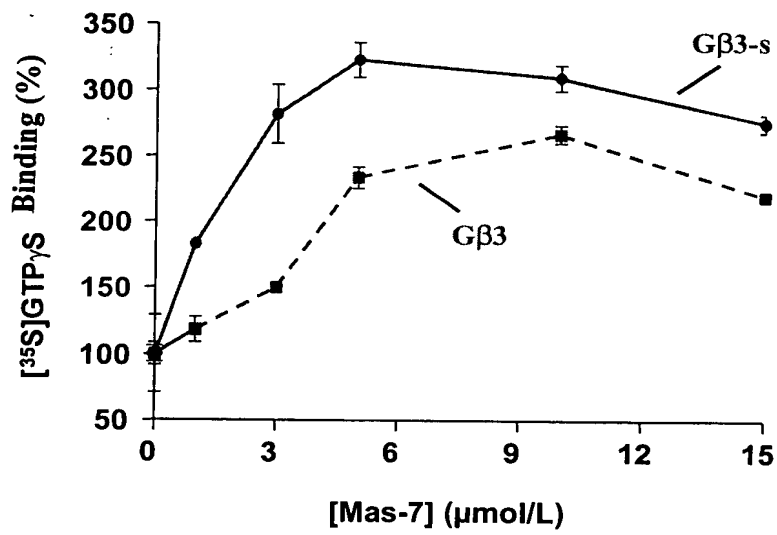


Fig. 2

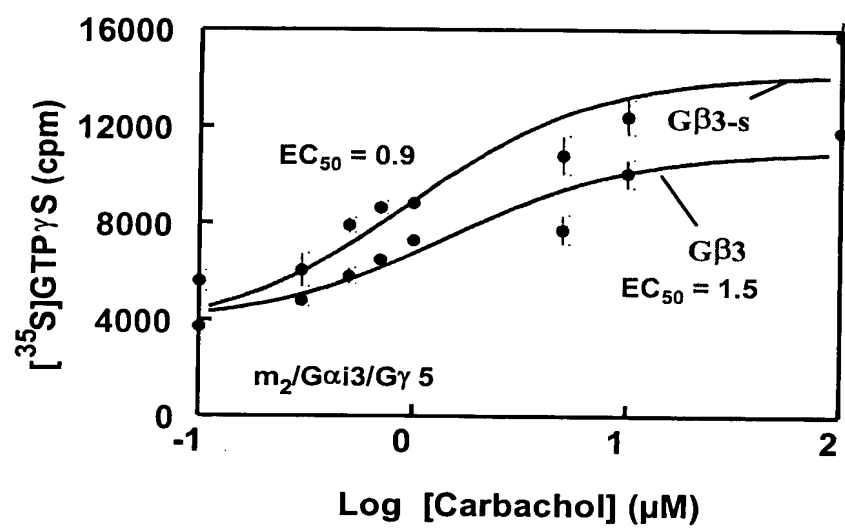


Fig. 3

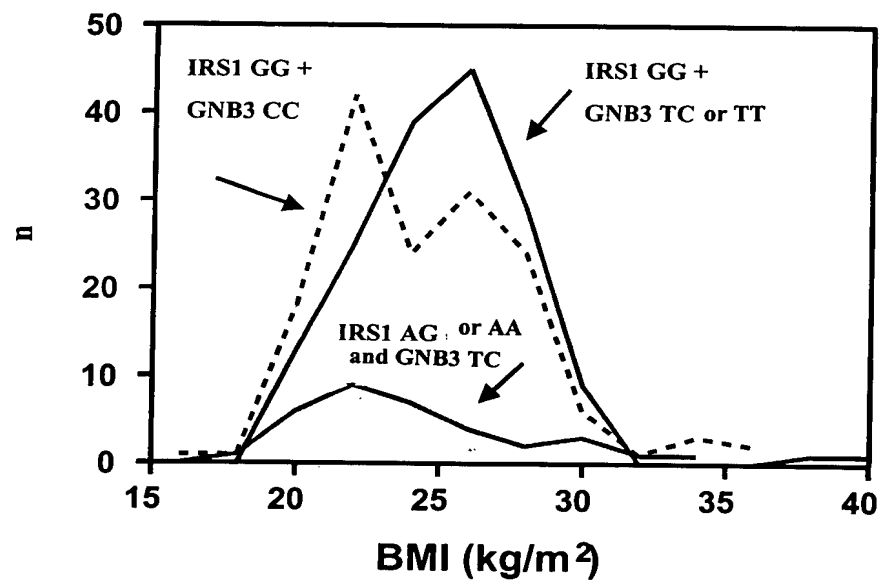


Fig. 4

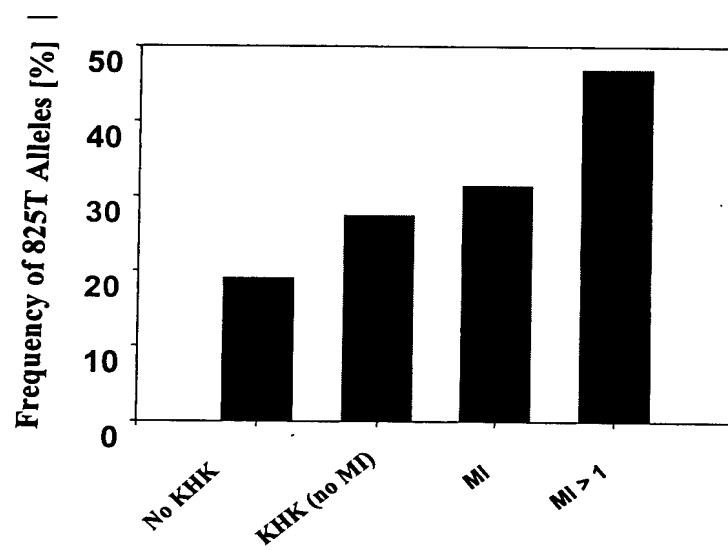


Fig. 5

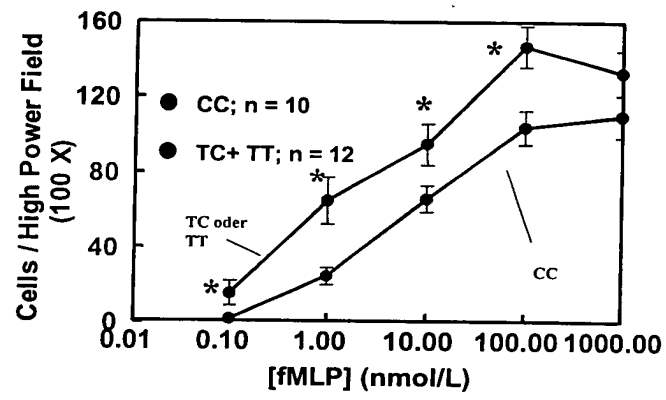


Fig. 6

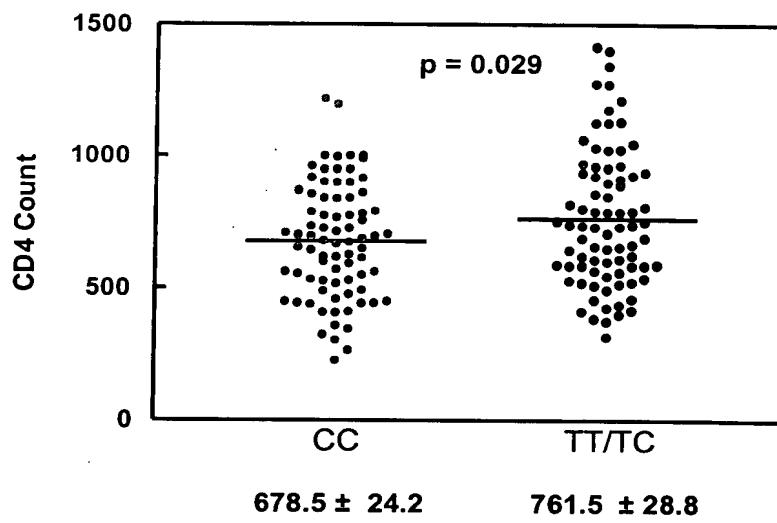


Fig. 7

### Enhanced Chemotaxis of T-Lymphocytes from 825T Allele Carriers

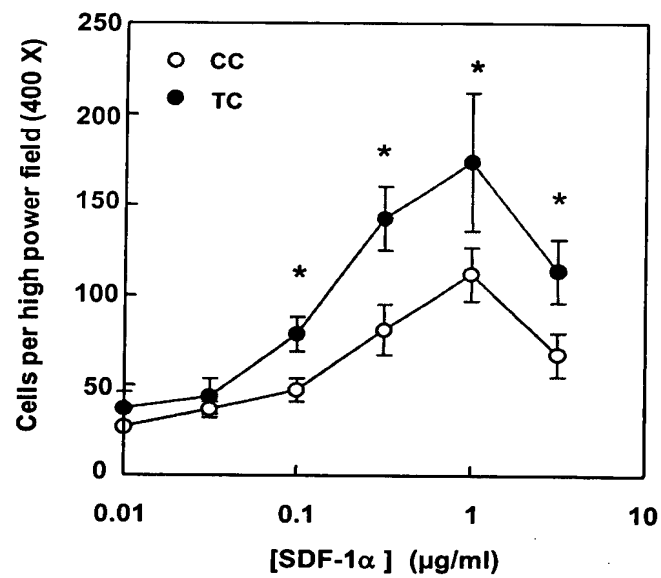


Fig. 8

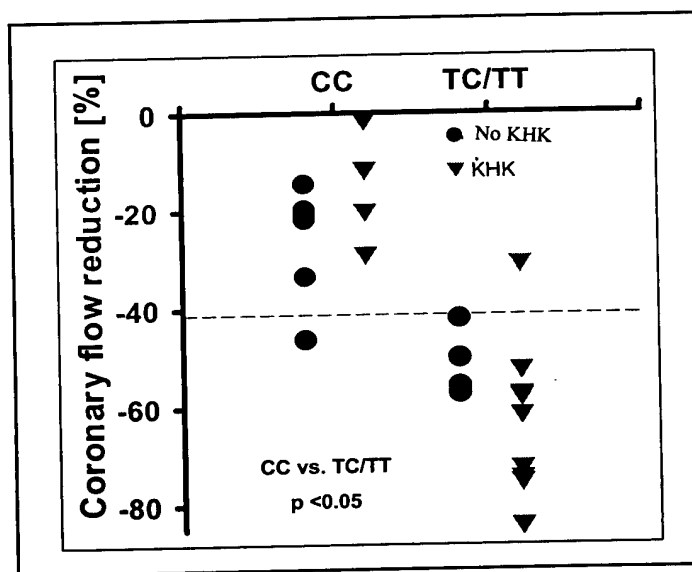




Fig. 9

# Time to AIDS

AIDS is defined as AIDS-defining disorders or CD4 count < 200

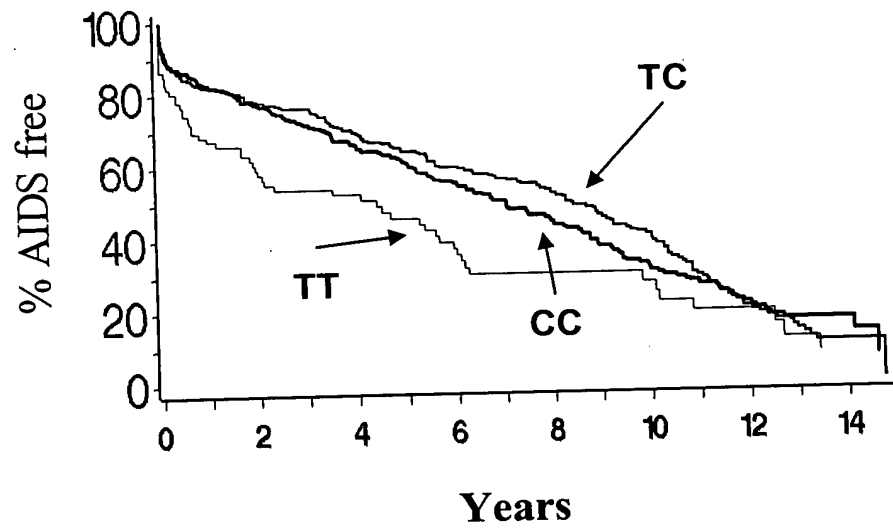


Fig. 10

**Event: CD4 Cell Count Below 200 per  $\mu$ l**

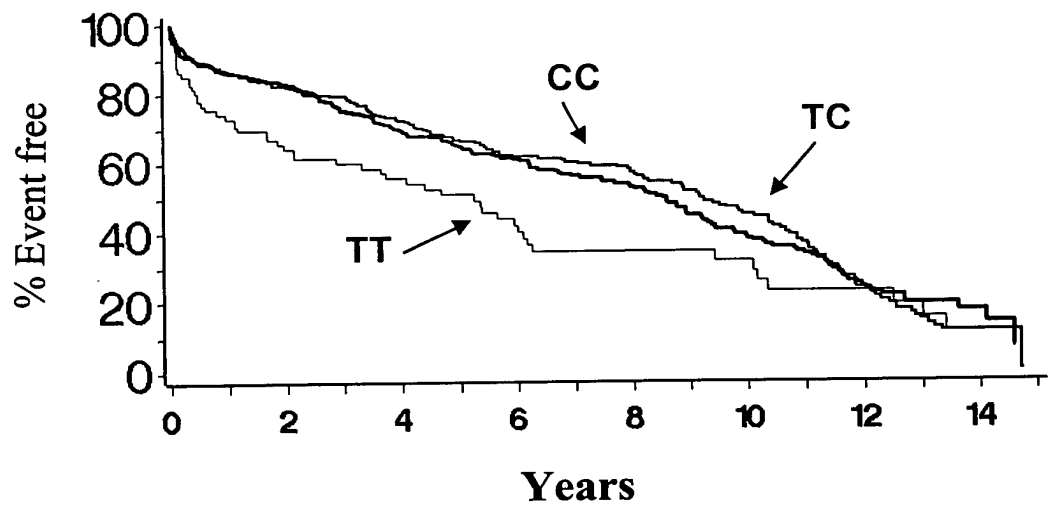


Fig. 11

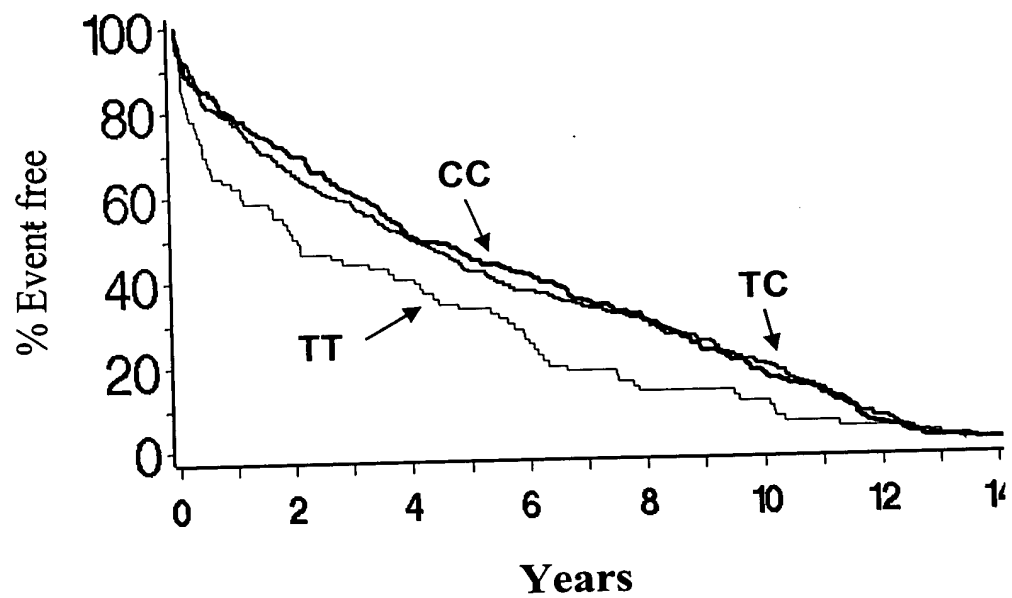
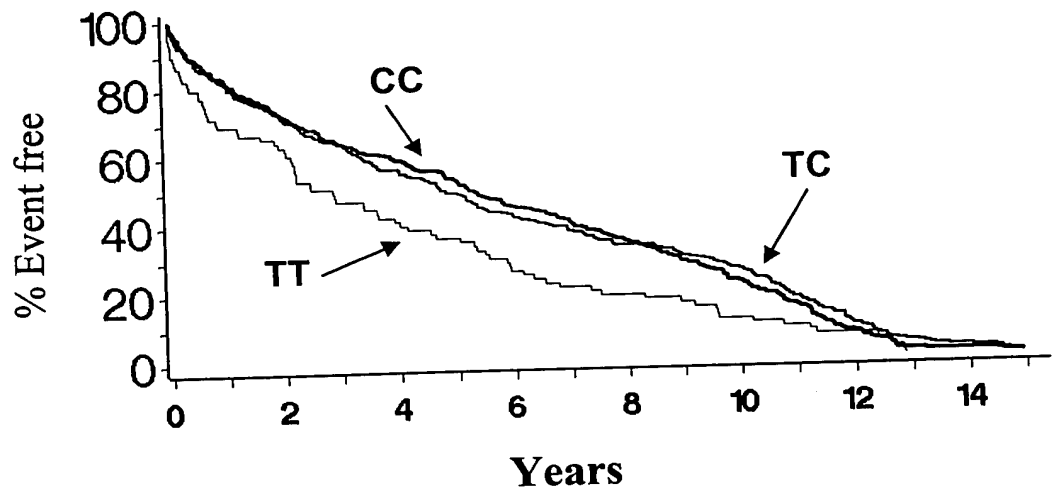
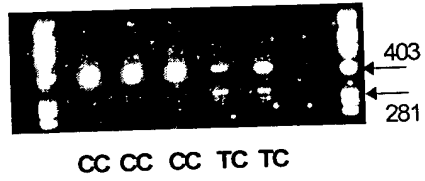
**Event: Lowest CD4 Cell Count**

Fig. 12

**Event: Time to maximum HIV Virus Load**  
Virus Copy Number determined by Quantitative PCR



.Fig. 13



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Fig. 14

### Potential Structures of G $\beta$ 3 and G $\beta$ 3s / G $\beta$ 3s-2

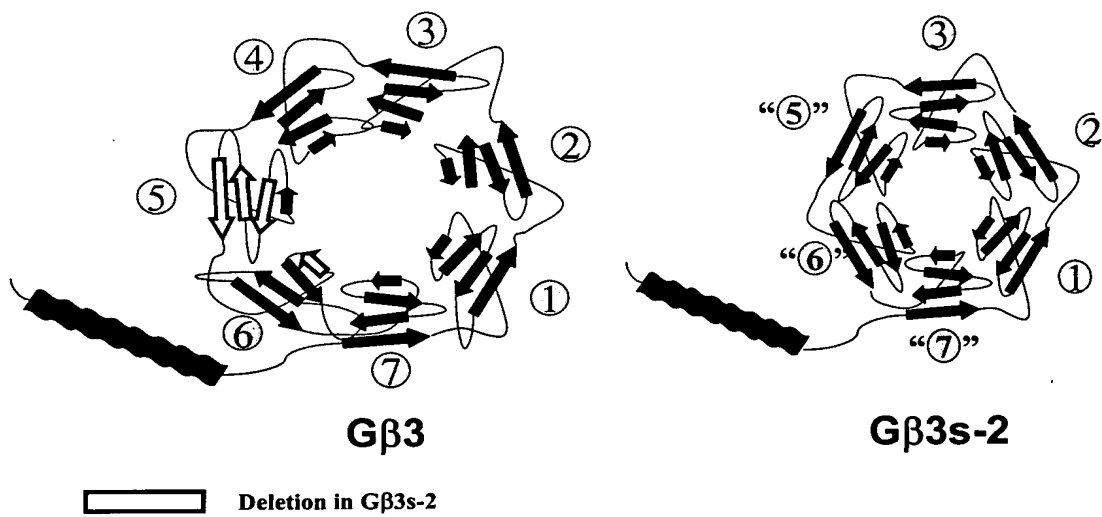


Fig. 15

1 Sf9 Cells  
varianten

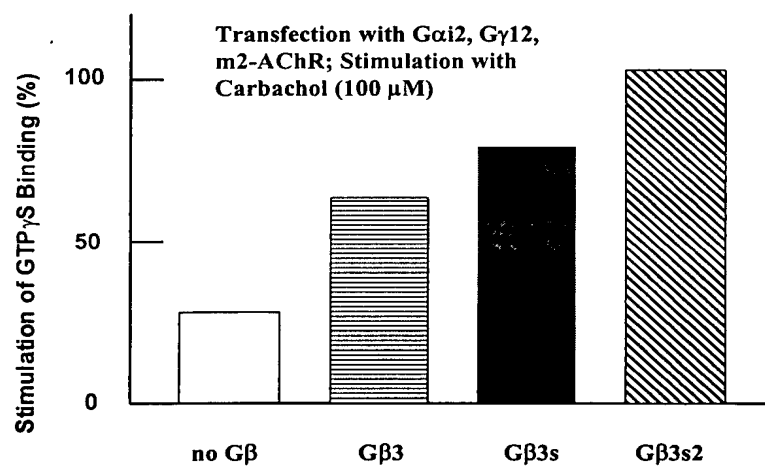


Fig. 16

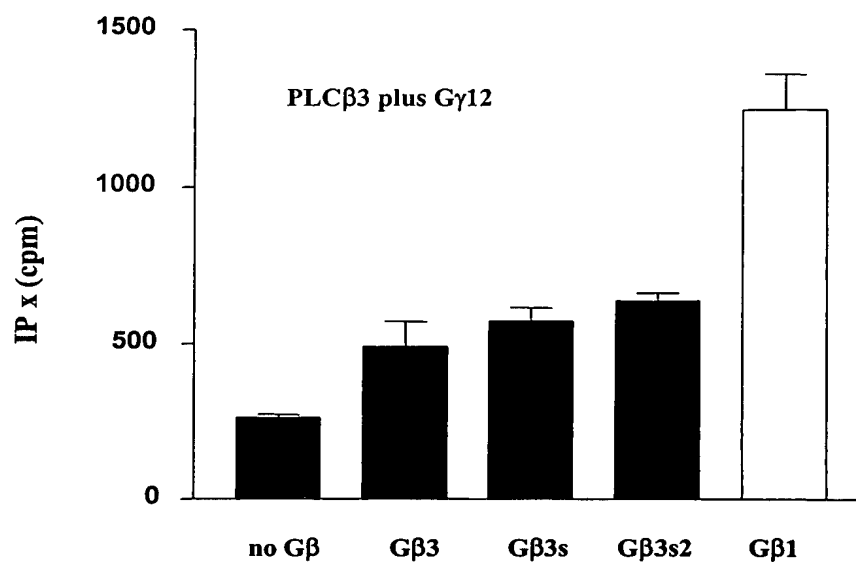




FIG. 17  $\beta$ 3-original sequence of Levine. The exons are underlined alternately. The area which is omitted by cryptic splice as bold-faced.

1 gggtcgATGG GGGAGATGGA GCAACTGCGT CAGGAAGCGG AGCAGCTCAA GAAGCAGATT  
 Start-ATG EXON 3 after Ansari-Lari  
 Nucleotide 1-6 seem not to be affected

61 GCAGATGCCA GGAAAGCCTG TGCTGACGTT ACTCTGGCAG AGCTGGTGTC TGGCCTAGAG  
 /Beginning EXON 4 /EXON 5 Beginning  
 ==> ENDE 1 KLON ANSARI

121 GTGGTGGGAC GAGTCCAGAT GCGGACGCGG CGGACGTTAA GGGGACACCT GGCCAAGATT  
 EXON 5

181 TACGCCATGC ACTGGGCCAC TGATTCTAAG CTGCTGGTAA GTGCCTCGCA AGATGGGAAG  
 EXON 5 / Beginning EXON 6

241 CTGATCGTGT GGGACAGCTA CACCACCAAC AAGGTGCAG CCATCCCCT GCGCTCCTCC  
 EXON 6 / EXON 7

301 TGGGTCATGA CCTGTGCCTA TGCCCCATCA GGGAACCTTG TGGCATGTGG GGGGCTGGAC  
 EXON 7

361 AACATGTGTT CCATCTACAA CCTCAAATCC CGTGAGGGCA ATGTCAAGGT CAGCCGGGAG  
 EXON 7

421 CTTCTGCTC ACACAGGTTA TCTCTCCTGC TGCCGCTTCC TGGATGACAA CAATATTGTG  
 EXON 7 /EXON 8

481 ACCAGCTCGG GGGACACCAC GTGTGCCTTG TGGGACATTG AGACTGGGCA GCAGAAGACT  
 EXON 8 /EXON 9

cryptic SPLICING

541 GTATTGTGG GACACACGGG TGACTGCATG AGCCTGGCTG TGTCTCCTGA CTCAATCTC  
 EXON 9  
 cryptic SPLICING

601 TTCATTTTCGG GGGCCTGTGA TGCCAGTGCC AAGCTCTGGG ATGTGCGAGA GGGGACCTGC  
 EXON 9  
 cryptic SPLICING /

661 CGTCAGACTT TACTGGCCA CGAGTCGGAC ATCAACGCCA TCTGTTTCTT CCCCAATGGA  
 EXON 9 / Beginning EXON 10

721 GAGGCCATCT GCACGGGCTC GGATGACGCT TCCTGCCGCT TGTTTGACCT GCGGGCAGAC  
 EXON 10

781 CAGGAGCTGA TCTGCTTCTC CCACGAGAGC ATCATCTGCG GCATCACGTC CGTGGCCTTC  
 EXON 10 Polymorphism site acgtc tgt

841 TCCCTCAGTG GCCGCCTACT ATTCGCTGGC TACGACGACT TCAACTGCAA TGTCTGGGAC  
 EXON 10

901 TCCATGAAGT CTGAGCGTGT GGGCATCCTC TCTGGCCACG ATAACAGGGT GAGCTGCCTG  
 EXON 10 /Beginning EXON 11

961 GGAGTCACAG CTGACGGGAT GGCTGTGGCC ACAGGTTCTT GGGACAGCTT CCTCAAAATC  
 EXON 11

1021 TGGAAGTGAq gaggtggag aaagggaggt ggaaggcagt gaacacactc agcagccccc  
 EXON 11  
 End of Open Reading Frame

1081 tgcccgaccc catctcattc aggtgttctc ttctatatc cgggtgccat tccactaag  
 EXON 11

1141 ctttctcctt tgagggcagt ggggagcatg ggactgtgcc tttgggaggc agcatcaggg  
 EXON 11

1201 acacaggggc aaagaactgc cccatctcct cccatggcct tccctcccca cagtcctcac  
EXON 11

1261 agcctctccc ttaatgagca aggacaacct gcccctcccc agccctttgc aggccagca  
EXON 11

1321 gacttgagtc tgaggcccca ggcctagga ttctccccc agagccacta cctttgtcca  
EXON 11

1381 ggcctgggtg gtatagggcg ttggccctg tgactatggc tctggcacca ctaggtcct  
EXON 11

1441 ggcctcttc ttattcatgc tttctccttt ttctaccttt tttctctcc taagacacct  
EXON 11

1501 gcaataaagt gtagcaccct ggt  
EXON 11 POLY A SITE

CCDS:03260

Fig. 18 Sequence with two polymorphisms (Numbering after the Levine sequence)

gggtcgatgg	gggagatgga	gcaactgcgt	caggaagcgg	agcagctcaa	gaagcagatt	60
gcagatgcc	ggaaagcctg	tgctgacgtt	actctggcag	agctggtgtc	tggcctagag	120
gtggtgggac	gagtccagat	gcggacgcgg	cggacgttaa	ggggacacct	ggccaagatt	180
tacgccatgc	actgggccac	tgattctaag	ctgctggtaa	gtgcctcgca	agatgggaag	240
ctgatcgtgt	gggacagcta	caccaccaac	aagggtgcacg	ccatcccact	gcgctcctcc	300
tgggtcatga	cctgtgccta	tgcccatca	gggaactttg	tggcatgtgg	ggggctggac	360
aacatgtgtt	ccatctacaa	cctcaaatcc	cgtgagggca	atgtcaagg	cagccgggag	420
ctttctgctc	acacaggtta	tctctcctgc	tgccgcttcc	tggatgacaa	caatattgtg	480
accagctcgg	gggacaccac	gtgtgccttg	tgggacattg	agactgggca	gcagaagact	540
gtatttgtgg	gacacacggg	tgactgcatg	agcctggctg	tgtctcctga	cttcaatctc	600
ttcatttcgg	gggcctgtga	tgccagtgcc	aagctctggg	atgtgcgaga	ggggacctgc	660
cgtcagactt	tacttgccca	cgagtcggac	atcaacgcca	tctgtttctt	ccccaatgga	720
gaggccatct	gcacgggctc	ggatgacgct	tcctgccgct	tgtttgacct	gcgggcagac	780
caggagctga	tctgcttctc	ccacgagagc	atcatctgcg	gcatcacgtc	tgtggccttc	840
tccctcagtg	gccgcctact	attcgctggc	tacgacgact	tcaactgcaa	tgtctgggac	900
tccatgaagt	ctgagcgtgt	gggcatcctc	tctggccacg	ataacagggt	gagctgcctg	960
ggagtcacag	ctgacgggat	ggctgtggcc	acaggttcct	gggacagctt	cctcaaaatc	1020
tggaaactgag	gaggctggag	aaagggaagt	ggaaggcagt	gaacacactc	agcagcccc	1080
tgcccgaccc	catctcattc	aggtgttctc	ttctatattc	cgggtgccat	tcccactaag	1140
ctttctcctt	tgagggcagt	ggggagcatg	ggactgtgcc	tttgggaggc	agcatcaggg	1200
acacaggggc	aaagaactgc	cccatctcct	cccatggcct	tccctcccca	cagtcctcac	1260
agcctctccc	ttaatgagca	aggacaacct	gcccctcccc	agccctttgc	aggcccagca	1320
gacttgagtc	tgaggcccca	ggccctagga	ttcctccccc	agagccacta	cctttgtcca	1380
tctggcacta	ctaggcctgg	gtggtatagg	gcgtttggcc	ctgtgactat	ggctctggca	1440
ccactagggg	cctggccctc	ttcttattca	tgctttctcc	tttttctacc	tttttttctc	1500
tcctaagaca	cctgcaataa	agtgtagcac	cctggg			1536

Fig. 19 Nucleic acid sequence of cDNA of G $\beta$ 3 and description of the deletion in G $\beta$ 3 and G $\beta$ 3s-2. Numbering referenced to the cDNA of Levine et al.(Levine, M.A., Smallwood, P.M., Moen, P.T., Jr., Helman, L.J., and Ahn, T.G. Molecular cloning of  $\beta$ 3 subunit, a third form of the G protein beta-subunit polypeptide.

*Proc.Natl.Acad.Sci.USA* 87(6):2329-2333, 1990) Here numbering does not begin with start codon ATG, but 6 nucleotides earlier in the 5' area.

```

1   gggtcgATGG GGGAGATGGA GCAACTGCGT CAGGAAGCGG AGCAGCTCAA GAAGCAGATT
    Start-ATG      EXON 3
    Nucleotide 1-6 seem not to be affected

61  GCAGATGCCA GGAAAGCCTG TGCTGACGTT ACTCTGGCAG AGCTGGTGTC TGGCCTAGAG
    /Beginn EXON 4                                /EXON 5 Beginning

121 GTGGTGGGAC GAGTCCAGAT GCGGACGCGG CGGACGTTAA GGGGACACCT GGCCAAGATT
    EXON 5

181 TACGCCATGC ACTGGGCCAC TGATTCTAAG CTGCTGGTAA GTGCCTCGCA AGATGGGAAG
    EXON 5                                / Beginning EXON 6

241 CTGATCGTGT GGGACAGCTA CACCACCAAC AAGGTGCACG CCATCCCCT GCGCTCCTCC
    EXON 6                                / EXON 7

301 TGGGTCATGA CCTGTGCCTA TGCCCCATCA GGGAACCTTG TGGCATGTGG GGGGCTGGAC
    EXON 7

361 AACATGTGTT CCATCTACAA CCTCAAATCC CGTGAGGGCA ATGTCAAGGT CAGCCGGGAG
    EXON 7

421 CTTTCTGCTC ACACAGGTTA TCTCTCCTGC TGCCGCTTCC TGGATGACAA CAATATTGTG
    EXON 7                                /EXON 8

```

481 ACCAGCTCGG GGGACACCAC GTG TGGGCTTG TGGGACATTG AGAGTGGGGA GCAGAGAGCT  
EXON 8 /EXON 9

501 TTTCAATTTCCTT CCGCCCTCTCTG TCCCACTGCCC AAGCTCTGGG ATGTGCGAGA GGGGACCTGCG

661 CGTCAGACTT TCACTGGCCA CGAGTCGGAC ATCAACGCCA TCTGTTT ~~CTT TGGCAATGCA~~  
 EXON 9 / Beginn EXON 10  
 Intron dazwischen 1607 bp

721 GAGGCCATCTTGCACGGGGCTC GGATGACGCT TCCTGCCGCT TGTTTGACCT GCGGGCAGAC  
EXON 10

781 CACGAGCTGA TGTGCTTCTG CCACGAGAGC ATGATCTGCG GATGACCTC CGTGCCCTT  
EXON 10 polymorphism site acgtc tgt

841 TCCCTCAGTG GCCGCCTACT ATTCGCTGGC TACGACGACT TCAACTGCAA TGTCTGGGAC  
EXON 10

901 TCCATGAAGT CTGAGCGTGT GGGCATCCTC TCTGGCCACG ATAACAGGGT GAGCTGCCTG  
EXON 10 /Beginning EXON 11 (Intron dazw. 989 bp)

961 GGAGTCACAG CTGACGGGAT GGCTGTGGCC ACAGGTCCT GGGACAGCTT CCTCAAATC  
EXON 11

1021 TGGAAGTGA gaggctggag aaaggggaagt ggaaggcagt gaacacactc agcagccccc  
EXON 11

End of Open Reading Frame B3-3

1081 tgcccgaccc catctcattc aggtgttctc ttctatattc cgggtgccat tcccactaag  
EXON 11

110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 1099 1100 1101 1102 1103 1104 1105 1

1141 ctttctcctt tgagggcagt ggggagcatg ggactgtgcc tttgggaggc agcatcaggg

EXON 11

1201 acacaggggc aaagaactgc cccatctcct cccatggcct tccctcccca cagtcctcac

EXON 11

1261 agcctctccc ttaatgagca aggacaacct gcccctcccc agccctttgc aggcccagca

EXON 11

1321 gacttgagtc tgaggcccca ggcctagga ttcctcccc agagccacta cctttgtcca

EXON 11

314231

tctggcac<sup>1</sup>a cta

1381 ggcctgggtg gtatagggcg tttggccctg tgactatggc tctggcac<sup>2</sup>a ctagggtcct

EXON 11

1441 ggccctcttc ttattcatgc tttctcctt ttctacctt tttctctcc taagacacct

EXON 11

1501 gcaataaagt gtagcaccct ggt

EXON 11 POLY A SITE

123456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100

atg	ggg	gag	atg	gag	caa	ctg	cgt	cag	gaa	gcg	gag	cag	ctc	aag	aag	48
Met	Gly	Glu	Met	Glu	Gln	Leu	Arg	Gln	Glu	Ala	Glu	Gln	Leu	Lys	Lys	
				5					10					15		
cag	att	gca	gat	gcc	agg	aaa	gcc	tgt	gct	gac	gtt	act	ctg	gca	gag	96
Gln	Ile	Ala	Asp	Ala	Arg	Lys	Ala	Cys	Ala	Asp	Val	Thr	Leu	Ala	Glu	
			20					25					30			
ctg	gtg	tct	ggc	cta	gag	gtg	gtg	gga	cga	gtc	cag	atg	cgg	acg	cgg	144
Leu	Val	Ser	Gly	Leu	Glu	Val	Val	Gly	Arg	Val	Gln	Met	Arg	Thr	Arg	
		35					40					45				
cgg	acg	tta	agg	gga	cac	ctg	gcc	aag	att	tac	gcc	atg	cac	tgg	gcc	192
Arg	Thr	Leu	Arg	Gly	His	Leu	Ala	Lys	Ile	Tyr	Ala	Met	His	Trp	Ala	
	50					55					60					
act	gat	tct	aag	ctg	ctg	gta	agt	gcc	tcg	caa	gat	ggg	aag	ctg	atc	240
Thr	Asp	Ser	Lys	Leu	Leu	Val	Ser	Ala	Ser	Gln	Asp	Gly	Lys	Leu	Ile	
65				70					75					75		
gtg	tgg	gac	agc	tac	acc	acc	aac	aag	gtg	cac	gcc	atc	cca	ctg	cgc	288
Val	Trp	Asp	Ser	Tyr	Thr	Thr	Asn	Lys	Val	His	Ala	Ile	Pro	Leu	Arg	
				80				85					90			
tcc	tcc	tgg	gtc	atg	acc	tgt	gcc	tat	gcc	cca	tca	ggg	aac	ttt	gtg	336
Ser	Ser	Trp	Val	Met	Thr	Cys	Ala	Tyr	Ala	Pro	Ser	Gly	Asn	Phe	Val	
		95					100					105				
gca	tgt	ggg	ggg	ctg	gac	aac	atg	tgt	tcc	atc	tac	aac	ctc	aaa	tcc	384
Ala	Cys	Gly	Gly	Leu	Asp	Asn	Met	Cys	Ser	Ile	Tyr	Asn	Leu	Lys	Ser	
		110			115				120							
cgt	gag	ggc	aat	gtc	aag	gtc	agc	cgg	gag	ctt	tct	gct	cac	aca	ggc	432
Arg	Glu	Gly	Asn	Val	Lys	Val	Ser	Arg	Glu	Leu	Ser	Ala	His	Thr	Gly	
	125				130				135							
tat	ctc	tcc	tgc	tgc	cgc	ttc	ctg	gat	gac	aac	aat	att	gtg	acc	agc	480
Tyr	Leu	Ser	Cys	Cys	Arg	Phe	Leu	Asp	Asp	Asn	Asn	Ile	Val	Thr	Ser	
140				145				150					155			
tcg	ggg	gac	acc	acg	tgt	gcc	ttg	tgg	gac	att	gag	act	ggg	cag	cag	528
Ser	Gly	Asp	Thr	Thr	Cys	Ala	Leu	Trp	Asp	Ile	Glu	Thr	Gly	Gln	Gln	
160				165				170						175		
aag	act	gta	ttt	gtg	gga	cac	acg	ggc	gac	tgc	atg	agc	ctg	gct	gtg	576
Lys	Thr	Val	Phe	Val	Gly	His	Thr	Gly	Asp	Cys	Met	Ser	Leu	Ala	Val	
				180				185					190			
ctc	cct	gac	ttc	aat	ctc	ttc	att	tcg	ggg	gcc	tgt	gat	gcc	agt	gcc	624
Ser	Pro	Asp	Phe	Asn	Leu	Phe	Ile	Ser	Gly	Ala	Cys	Asp	Ala	Ser	Ala	
			195				200						205			

